

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in this application.

Listing of Claims:

Claims 1 through 70 (Cancelled)

71. (New) A method for identifying a ligand that binds to a protein, comprising the steps of:

(1) receiving unfolding data that indicates thermal unfolding as a function of temperature for a protein incubated with a molecule tested for binding;

(2) determining an unfolding temperature midpoint for the protein in the presence of the molecule from the unfolding data;

(3) comparing the unfolding temperature midpoint for the protein incubated with the ligand with the unfolding temperature midpoint for the protein in the absence of any molecules tested for binding; and

(4) determining that the molecule tested for binding binds to the protein when a difference between the unfolding temperature midpoint for the protein in the presence of the molecule and unfolding temperature midpoint for the protein in the absence of any molecules tested for binding exceeds a threshold; and

(5) estimating the ligand binding affinity at the unfolding temperature midpoint according to:

$$K_L^{T_m} = \frac{\exp\left\{-\frac{\Delta H_u^{T_0}}{R}\left[\frac{1}{T_m} - \frac{1}{T_0}\right] + \frac{\Delta C_{pu}}{R}\left[1n\left(\frac{T_m}{T_0}\right) + \frac{T_0}{T_m} - 1\right]\right\}}{[L_{T_m}]}$$

where,

$K_L^{T_m}$ is a ligand association constant at T_m ;

T_m is a midpoint temperature for the protein unfolding transition in the presence of the ligand;

T_0 is a midpoint temperature for the protein unfolding transition in the absence of the ligand;

$\Delta H_u^{T_0}$ is an enthalpy of protein unfolding in the absence of ligand at T_0 ;

ΔC_{pu} is a change in heat capacity upon protein unfolding in the absence of ligand;

$[L_{T_m}]$ is a free ligand concentration at T_m ; and

R is the gas constant.

72. (New) The method according to claim 71, further comprising the step of:

(6) inserting actual values $\Delta H_u^{T_0}$ and ΔC_{pu} into the equation of step (5)

73. (New) The method according to claim 71, further comprising the step of:

(6) estimating values for $\Delta H_u^{T_0}$ and ΔC_{pu} for use in the equation of step (5)

74. (New) The method according to claim 73, wherein step (6) comprises the steps of:

(a) fitting the data with a least squares algorithm according to:

$$y(T) = y_u + \frac{(y_f - y_u)}{1 + \exp \left[\left[\frac{-\Delta H_u}{R} \right] \left[\frac{1}{T} - \frac{1}{T_m} \right] + \left[\frac{\Delta C_{pu}}{R} \right] \left[\left(\frac{T_m}{T} - 1 \right) + 1n \frac{T}{T_m} \right] \right]}$$

where,

$y(T)$ is fluorescence unfolding data as a function of temperature T ;

y_u is a pre-transitional fluorescence intensity,

y_f is a post-transitional fluorescence intensity;

ΔH_u is a protein unfolding enthalpy;

ΔC_{pu} is a change in heat capacity upon protein unfolding;

T_m is a midpoint temperature for protein unfolding transition in the presence of the ligand; curve fit

(b) varying values for y_u , y_f , ΔH_u , ΔC_{pu} , and ΔC_{pu} until a suitable is obtained; and

(c) using resultant values from step 9(b) in step (5).

75. (New) The method according to claim 71, further comprising the step of:

(6) determining a ligand binding constant, for any temperature T , according to:

$$K_L^T = K_L^{T_m} \exp \left\{ -\frac{\Delta H_L^T}{R} \left[\frac{1}{T} - \frac{1}{T_m} \right] + \frac{\Delta C_{pL}}{R} \left[\ln \left(\frac{T}{T_m} \right) - \frac{T}{T_m} + 1 \right] \right\}$$

76. (New) A method for identifying a ligand that binds to a protein, comprising the step of:

- (1) receiving unfolding data that indicates thermal unfolding as a function of temperature for a protein incubated with a molecule tested for binding;
- (2) determining an unfolding temperature midpoint for the protein in the presence of the molecule from the unfolding data;
- (3) comparing the unfolding temperature midpoint for the protein incubated with the ligand with the unfolding temperature midpoint for the protein in the absence of any molecules tested for binding; and
- (4) determining that the molecule tested for binding binds to the protein when a difference between the unfolding temperature midpoint for the protein in the presence of the molecule and unfolding temperature midpoint for the protein in the absence of any molecules tested for binding exceeds a threshold; and
- (5) estimating the ligand binding affinity at the unfolding temperature midpoint; and
- (6) determining a ligand binding constant, for any temperature T, according to:

$$K_L^T = K_L^{T_m} \exp \left\{ -\frac{\Delta H_L^T}{R} \left[\frac{1}{T} - \frac{1}{T_m} \right] \right\}$$

77. (New) The method according to claim 75, wherein step (1) further comprises the step of plotting thermal unfolding according to a non-linear, least square fitting algorithm.